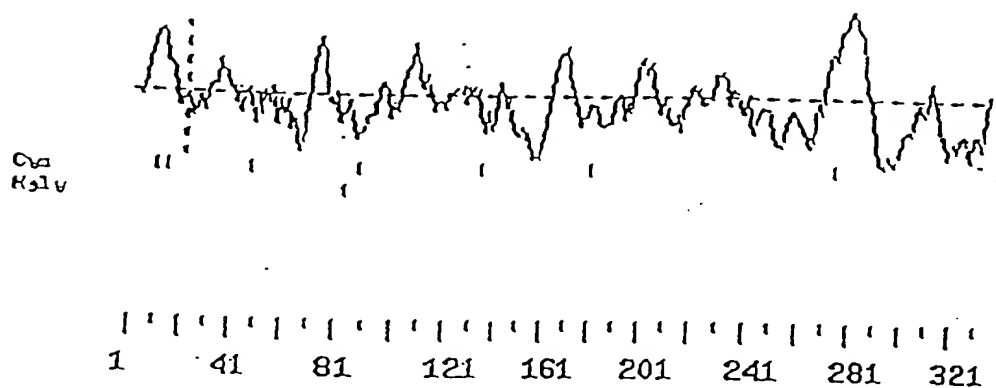


GGAGTCGACCCACGGCTCCGACAGGGCTGAGGAACC	H S P S P T A L F C L	11
ATG TCT CCA TGC CCG ACC GCC CTC TTC TGT CTT		68
G L C L G R V P A Q S G P L P K P S L Q		31
GGG CTC TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG		128
A L P S S L V P L E K P V T L R C Q G P		51
GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT		188
P G V D L Y R L E K L S S S R Y Q D Q A		71
CCG GGC GTG GAC CTG TAC CCG CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA		248
V L F I P A H K R S L A G R Y R C S Y Q		91
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CCG TAC CGG TGC TCC TAC CAG		308
N G S L W S L P S D Q L E L V A T G V F		111
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT		368
A K P S L S A Q P G P A V S S G G D V T		131
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC		428
L O C Q T R Y G F D Q F A L Y K E G D P		151
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT		488
A P Y K N P E R W Y R A S F P I I T V T		171
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CCG GCT AGT TTC CCC ATC ATC ACG GTG ACC		548
A A H S G T Y R C Y S F S S R D P Y L W		191
GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG		608
S A P S D P L E L V V T G T S V T P S R		211
TGG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG		668
L P T E P P S S V A E F S E A T A E L T		231
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC		728
V S F T N K V F T T E T S R S I T T S P		251
GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA		788
K E S D S P A G P A R Q Y Y T K G N L V		271
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC		848
R I C L G A V I L I I L A G F L A E D W		291
CGG ATA TGC CTC GGG GCT GTG ATC CTA ATA ATC CTG GCG GGG TTT CTG GCA GAG GAC TGG		908
H S R R K R L R H R G R A V Q R P L P P		311
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC		968
L P P L P Q T R K S H G G Q D G G R Q D		331
CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT		1028
V H S R G L C S *		340
GTT CAC AGC CGC GGG TTA TGT TCA TGA		1055

FIGURE 1a



MSPSP TALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE
KLSSSR YQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRC
YSESSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT
TETSR SITTS PKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIGURE 2

ALIGN calculates a global alignment of two sequences
 version 2.0u Please cite: Myers and Miller, CABIOS (1989)
 > U91928 ORF 1893 aa vs.
 > hT268 ORF 1017 aa
 scoring matrix: paml20.mat, gap penalties: -12/-4
 37.7% identity; Global alignment score: -8

```

      10      20      30      40      50      60      70
inputs ATGACGCCCCGCTCACAGCCCTGCTCTGGCTTGGGCTGAGTCTGGGCCCCAGGACCCGCTGCAGGCAG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
      ATGTCTCCATCCCCGACCGCCCTCTTCTGTCTTGGGCTGTGTCTGGGCGG-TGTGCCAGC--GCAGAGTC
      10      20      30      40      50      60

      80      90      100      110      120      130
inputs GGGCCTTCCCCAAACCCACCCCTCTGGGCTGAGCCAGGCTCTGTGAT-CAGCTGGGGAGCCCCGTGACCA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
      GACCGCTCCCAAGCCCTCCCTCCAGGCTCTGCCCAGCTCCCTGGTGGCCCTGGAGAAGCCA-GTGACCC
      70      80      90      100      110      120      130

      140      150      160      170      180      190      200
inputs TCTGGTGTACAGGGAGCCCTGGAGGCCAGGAGTACCGACTGGATAAAGAGGGAAGCCAGAGCCCTTGA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
      TCCGGTGCCAGG--ACCT-----CCGGGCGTG--GACCTGTA-----CCGCTCGAG-----AAG
      140      150      160      170      180

      210      220      230      240      250      260      270
inputs CAGAAATAACCCACTGGAACCCAAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
      CTGAGTT--CCAGCAGGTACC-AGGATCA-GGCAGTCTCTTCATCCCCGCATGAAGAGAAGTCTGGCT
      190      200      210      220      230      240

      280      290      300      310      320      330      340
inputs GGGAGATACCGCTGCCACTATTACAGCTCTGCAG--GCTGGTCAGAGCCCAGCGACCCCTGGAGCTGGT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
      GGACGCTACCGCTGCTCCTAC--CAGAACGGAAGCCCTCTGGTCCCTGCCAGCGACCCAGCTGGAGCTCGT
      250      260      270      280      290      300      310

      350      360      370      380      390      400      410
inputs GATGACAGGATTCTACAACAAACCCACCCCTCTCAGCCCTGCCAGCCCTGTGGTGGCTCAGGGGGGAAT
      . :: :: :: :: . :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
      TGCAAGGGAGTTTTTGCCAAACCCCTCGCTCTCAGCCAGCCCGGCCCGGGTGTGTCTCAGGAGGGGAC
      320      330      340      350      360      370      380

      420      430      440      450      460      470      480
inputs ATGACCCCTCCGATGTGGCTCACAGAAGGATATCACCATTGTTCTGATGAAGGAAGGAGAACACCAGC
      . :: :: :: :: . :: :: :: :: . :: :: :: :: . :: :: :: :: . :: :: :: :: . :: :: :: ::
      GTAACCTACAGTGTACAGACTGGGTATGGCTTTGACCAATTTGCTCTGTACAGGAAGG-----
      390      400      410      420      430      440

      490      500      510      520      530      540      550
inputs TCCCCCGGACCCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCGCTGTTCCTGTGGGGCCCCGT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
  
```

FIGURE 3a

FIGURE 3b

FIGURE 3c

```
      1750      1760      1770      1780      1790      1800      1810
inputs TGAGGCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGG
      :::      :::      :::::      :::::      :::::      :::::      ::
      ---GCC---CGAC-----AGGATGTT-----CACAGC-----CG-
                                990                                1000

      1820      1830      1840      1850      1860      1870      1880
inputs AAGGCAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGG
      :::::      :::::      :::::      :::::      :::::      :::::      ::
      -----CGGGTTATG-----TTCA-----
                                1010

      1890
inputs CCATCCAC
      -----
```

FIGURE 3d

ALIGN calculates a global alignment of two sequences
 version 2.0u Please cite: Myers and Miller, CABIOS (1989)
 > ht268 a.a. 339 aa vs.
 > GenPept U91928 - Human clone HL9 monocyte inhib 631 aa
 scoring matrix: pam120.mat, gap penalties: -12/-4
 23.0% identity; Global alignment score: -642

```

      10      20      30      40      50      60
inputs MSPSPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSSLVPLEKPVTLRCQGPVVDLYRLEKLSSS---
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
      MTPALTALLCLCLSLGPRTRVQAGFPKPTLWAEPGSVISWGSPTIWCQGSLEAQEYRLDKEGSPEPLD
      10      20      30      40      50      60      70

      70      80      90      100     110     120     130
inputs RYQ----DQAVLFIPAKKRSLAGRYRCSYQNGSLHSLPSDQLELVATGVFAKPSLSAQPGPAAVSSGCDV
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
      RINPLEPKKXARFSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVHTGFYNKPTLSALPSPVVASCGNH
      80      90      100     110     120     130     140

inputs TLQCQT-----RY-----
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
      TLRCGSQKGYHHFVLMKEGEHQLPRTLDQQLHSGGFQALFPVGPVNPNSHRWRFTCYYYYHNTFPQVWSHP
      150     160     170     180     190     200     210

inputs -----GFDQFALYKEGDP-----
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
      SDPLEILPSCGVSRRKPSLLTLQCPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPQGQPQAGLSQAN
      220     230     240     250     260     270     280

inputs -----APYK-----HP-----ERW-----
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
      FILGPVSPSHGQYRCYCAHNLSSSEHSAPSOPNLILHAGQIYDTVSLSAQPGPTVASGENVTLLCQSHWQ
      290     300     310     320     330     340     350

inputs -----YRASFPITVTAAHSGTYRCYSFSSROPYLHSAFSDPLELVVTG
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
      FDTFLLTKEGAHPPFLRLRSHYGAKYQAEFPHSPVTSAHAGTYRCYGSYSSNPHLSPFPSEPLELHVSG
      360     370     380     390     400     410     420

      210     220     230     240     250     260
inputs TSVTPSRLPTEPPSS--VAEFSEATAELTVSFTNKVF-----TTETSRISITSPKESD--SPAGPA--
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
      HSCGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLFLLFLLLRQRHSHKRTSDQRKTDQRPAGAAE
      430     440     450     460     470     480     490

      270     280     290
inputs RQYYTKGNLVRICLGAVIL-----IILACFLAEDH-----HSRRKR-----
      .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:. .:.
  
```

FIGURE 4a

[illegible][illegible][illegible][illegible]

Alignments of top-scoring domains:

ig: domain 1 of 2, from 41 to 90: score 4.1, E = 6.1

```

      *->GesvtLtCsvgfgppgvsvtWYfkngk.lgpsllgysysrlesgek
ht268 41  .+ vTL+C+          + v Y + k ++          .R++ +
      EKPVTLRCCGP-----PGVDLY-RLEKISSS-----RYQDQ-- 70
      anlsegrfsissltLtissvekeDsGtYtCvWk--
ht268 71  ++L i      +++ +G Y+C
      -----AVLFIPAMKRSLAGRYRCSY      90

```

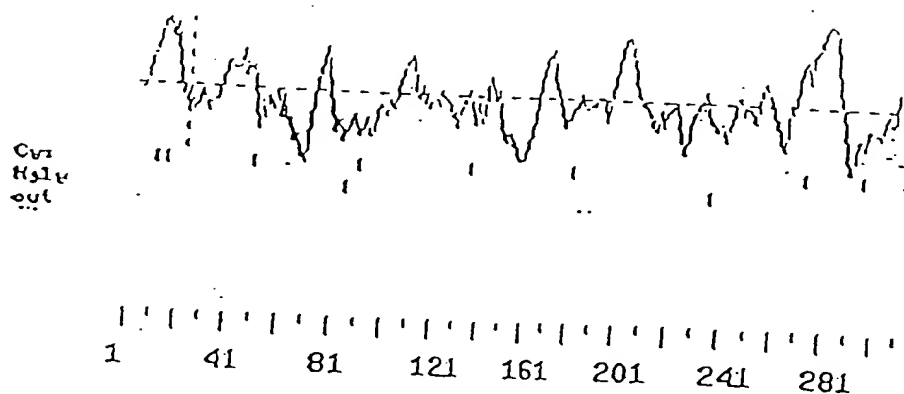
FIGURE 5A

ig: domain 2 of 2, from 127 to 182: score 19.1, E = 0.1
*->GesvtLtCsvsgfgppgvsvtWYfkngk.lgpsllgysysrlesgek
G++vtL+C+++ + ++ y k+g++ + y+++
hT268 127 GGDVTLQCQTR---YGFDDQFALY-KEGDpAP-----YKNPERWYR-- 162
anlsegrfsissltLtissvekeDsGtYtCw<-*
++++i++v++ sGtY+C
hT268 163 -----ASFPIITVTAHSGTYRCYS 182

FIGURE 5B

GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACCC ATG TCT CCA GCC 74
 S P T F F C I G L C V L Q V I O T Q S G 24
 TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC 134
 P L P K P S L Q A Q P S S L V P L G Q S 44
 CCA CTC CCC AAG CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT CAG TCA 194
 V I L R C Q G P P D V D L Y R L E K L K 64
 GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA 254
 P E K Y E D Q D F L F I P T H E R S H A 84
 CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT 314
 G R Y R C S Y Q N G S H W S L P S D Q L 104
 GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT 374
 E L I A T G V Y A K P S L S A H P S S A 124
 GAG CTA ATT GCT ACA GGT GTG TAT CCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA 434
 V P Q G R D V T L K C Q S P Y S F D E F 144
 GTC CCT CAA GGC AGG GAT GTG ACT CTC AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC 494
 V L Y K E G D T G P Y K R P E K W Y R A 164
 GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC 554
 N F P I I T V T A A H S G T Y R C Y S F 184
 AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC 614
 S S S S P Y L W S A P S D P L V L V V T 204
 TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT 674
 G L S A T P S Q V P T E E S F P V T E S 224
 GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA GAA TCA TTT CCT GTG ACA GAA TCC 734
 S R R P S I L P T H K I S T T E K P H N 244
 TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT 794
 I T A S P E G L S P P I G F A H Q H X A 264
 ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC 854
 K G N L V R I C L G A T I I I I L L G L 284
 AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT 914
 L A E D W H S R K K C L Q H R H R A L Q 304
 CTA GCA GAG GAT TGG CAC AGT CCG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA 974
 R P L P P L P L A 314
 AAG CCA CTA CCA CCC CTC CCA CTG GCC TAG 1004
 AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAAACCATGGACATCACCCTAGAGCCACAGACAT 1083
 GGACATACTCAAGAGTGGGGAGGTTATATATAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAAACAGGTGAAAAAAA 1162
 A 1163

FIGURE 6



MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIP TMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLCQSPYSFDEFVLYKEGDTGPKRPEKWYRANFPIITVTAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE
KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIGURE 7

ALIGN calculates a global alignment of two sequences
 version 2.0. Please cite: Myers and Miller, CABIOS (1989)
 > U91928 ORF 1893 aa vs.
 > mT268 ORF 939 aa
 scoring matrix: pam120.mat, gap penalties: -12/-4
 34.3% identity; Global alignment score: -836

```

      10      20      30      40      50      60      70
inputs ATGAGCGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCCGTGCAGGCCAG
      :::: :: :::: :::: :::: :::: ::::
      ATGTCTCCAGCC-TCAC--CC---ACTTCTTT--CTGTAT-----
      10      20      30

      80      90      100      110      120      130      140
inputs GGCCTTCCCCAAACCCACCCCTCTGGGCTGAGCCAGGCTCTGTGATCAGCTGGGGGAGCCCCCGTGACCAT
      :::::
      -----TGGGCTG-----TGTTACTGC-----
      40

      150      160      170      180      190      200      210
inputs CTGGTCTCAGGGGAGCCCTGGAGGCCACGAGTACCGACTGGATAAAGAGGGGAAGCCCCAGAGCCCTTGGAC
      :::::
      -----AAGTGATCC-----AAACACAGAG-----TGG--
      50      60      70

      220      230      240      250      260      270      280
inputs ACAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCGG
      :::::
      -----CCCACT--CCC--CAAG-----CCTTCCC-TCCAGG-----
      80      90

      290      300      310      320      330      340      350
inputs GGAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCGACCCCTGGAGCTGGTGAT
      : ::::
      -----CTCAGCC-----CAGTTCCCTG-GTACCCCTGGGTGAG-----
      100      110      120

      360      370      380      390      400      410      420
inputs GACAGGATTCTACAACAAACCCACCCCTCTCAGCCCTGCCAGCCCTGTGGTGGGCTCAGGGGGGAATATG
      .::: :: :::
      -TCAG--TTATTC-----TGAGGTG-C--CAGGGA-----
      130      140      150

      430      440      450      460      470      480
inputs ACCCTCC-GATGTGGCTCACAGAAGGGATATCAACATTTTGTCTGATGAAGGAAGGAGAACACCAGCTC
      :::: :::::
      --CCTCCAGATGTG--ATTTATATGGCTGGAGAAACTGAAA-----
      160      170      180      190

      490      500      510      520      530      540      550
inputs CCCCCGAOCCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCTGTGGGCCCCGTGA
      :::: ::
      :::: ::::: :::: ::::: :::: ::::
  
```

FIGURE 8a

FIGURE 8b

FIGURE 8c

FIGURE 8d

[illegible]

```

inputs TLKC--QSPY-----
      :: : :
      TLRCGSGKGYHMFVLKKEGEHQLPRTLDSQLHSGGFQALFPVGPVNPSSHRWRFTCYYYYYHITPQVWSE?
            150          160          170          180          190          200          210

```

```

inputs -----140      150
              -SFDEFVLYKEG-----
              ...:.....
SOPLEILPSGVSRKPSLLTLQGPVLAPQSLTLQCGSDVGYORFVLYKEGERDFLQRPQQPQAGLSQAN
      220      230      240      250      260      270      280

```

inputs -----TGPKY-----RP-----EKK-----160
 :::
FTLGPVSPSHCGQYRCYGHNLSSEHSAPSDPLNHLHAGQIYDTVSLSAQPGPTVASGENVTLLCQSHWQ
 290 300 310 320 330 340 350

```

              170      180      190      200
Inputs -----YRANFPFIITVTAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVVG
               :::::  :::::  :::::  :::::
FDTLLLTKEGAHPPLRLRSMYGAKKYQAEFPSPVTSAHAGTYRCYGSYSSNPRLSFPSEPLELVHG
           360       370       380       390       400       410       420

```

Inputs LSATPSQVPTES-----FPV-----
 .: .: .:
HSGCGSSLPPTGPPSTPGLGRYLEVLICGVSAFVLLLFI LLFLLRRQRHSKHRTSDQRKTDQFRPAGAAE
 430 440 450 460 470 480 490

Inputs

.	230	240	250	260	270
TESS-----RRPS-----ILPTNKISTEKPHNI-TASPEGLSP-PIGFAH--QHYAKGNLVR-I					
:: :::		. . . : . :	. . . : :	: . . :	:

FIGURE 9a

三

FIGURE 9b

Alignments of top-scoring domains:

ig: domain 1 of 2, from 42 to 91: score 10.2, E = 1.4

```

      *-->GesvtLtCsvgfgpppgvsvtkyfkngk.lgpsllgysysrlesgek
      G+sv L+C+      ++v Y + k ++      +++e +
nt268  42  QGSVILRCQGP-----PDVDLY-RLEKLRP-----EKYEDQ-- 71
      anlsegrfsissltLtissvekeDsGtYtCvv<--
      L i + e++++G Y+C
nt268  72 -----DFLFIPThERSNAGRYRCSY      91

```

FIGURE 10A .

ig: domain 2 of 2, from 128 to 183: score 9.6, E = 1.6
->GesvtLtCsvgfgppgvsvtwyfkngk.lgpsllgysysrlesgek
G +vtL C++ ++. y k+g++ + y+r+e +
DT268 128 GRDVTCLKQSP---YSFDEFVLY-KEGDtGP-----YKRPEKW-Y 162
anlsegrfsissltLtissvekeDsGtYtCvv<-.
+ ++i++v++ sGtY+C
DT268 163 RA-----NFPIITVTAHSGTYRCYS 183

FIGURE 10B

ALIGN calculates a global alignment of two sequences
 version 2.0 Please cite: Myers and Miller, CABIOS (1989)
 > ht268 a.a. 339 aa vs.
 > nt268 a.a. 313 aa
 scoring matrix: pen20.mat, gap penalties: -12/-4
 64.4% identity: Global alignment score: 1011

```

      10      20      30      40      50      60
inputs HSPSPALFCIGLCGRV-PHSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLEKLSSSRYQD
      .....
      HSPASPTFFCIGLCVLOVIQTSGPLPKPSLQALPSSLVPLGQSVILRCQGPVVDLYRLEKLSPEKYED
      10      20      30      40      50      60      70

      70      80      90      100     110     120     130
inputs QAVLFIPAKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYG
      .....
      QDFLFIPAKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAHPSSAVPQGRDVTLCQCTRYG
      80      90      100     110     120     130     140

      140     150     160     170     180     190     200
inputs FDQFALYKEGDPAPYKINPERWYPASFPITVTAHSGTYRCYSFSSRDPLYWSAPSDPLELVVTGTSVTP
      .....
      FDEFVLYKEGDTGPYKRPEKWRANFPITVTAHSGTYRCYSFSSSPYLSAPSDPLVLVVTGLSATP
      150     160     170     180     190     200     210

      210     220     230     240     250     260     270
inputs SRLPTEPPSSVAEFSEATAELTVSFTNKVTTETSRISITSPKESDSPAGPARQYYTKGNLVRICLGAVI
      .....
      SQVPTESFPVTESRRPSILP---TNKISTEKPNITASPEGLSPPIGFAHQHYAKGNLVRICLGATI
      220     230     240     250     260     270

      280     290     300     310     320     330
inputs LIILAGFLAEDWHSRRKRLRHGRGRAVQRPLPLPLPQTRKSHGGQDGGQDVSRLGLCS
      .....
      IIILGLAEDWHSRRKRLRHGRGRAVQRPLPLPLP-LA-----
      280     290     300     310

```

FIGURE 11

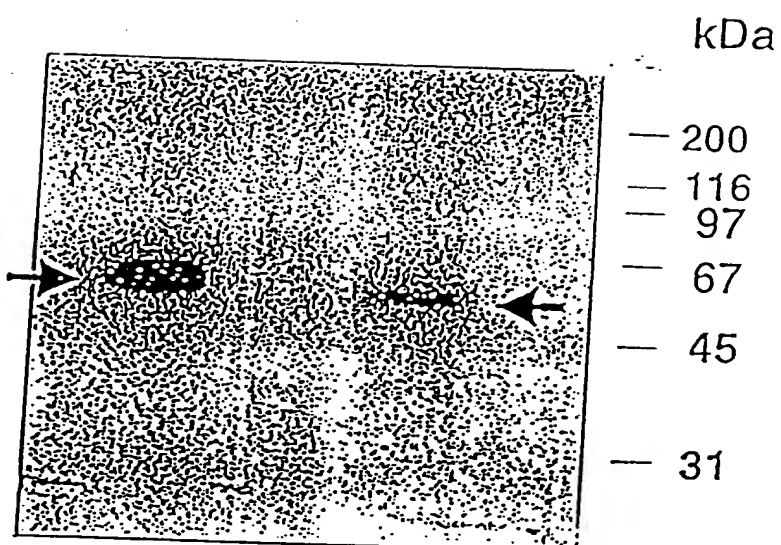
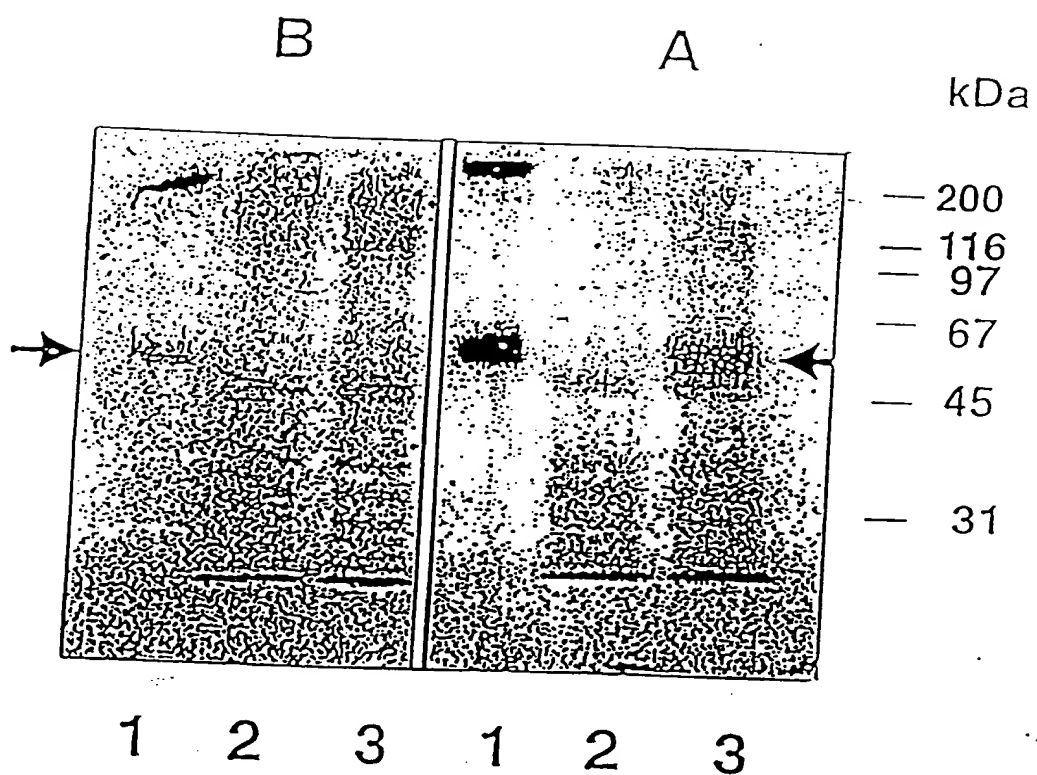


FIGURE 12



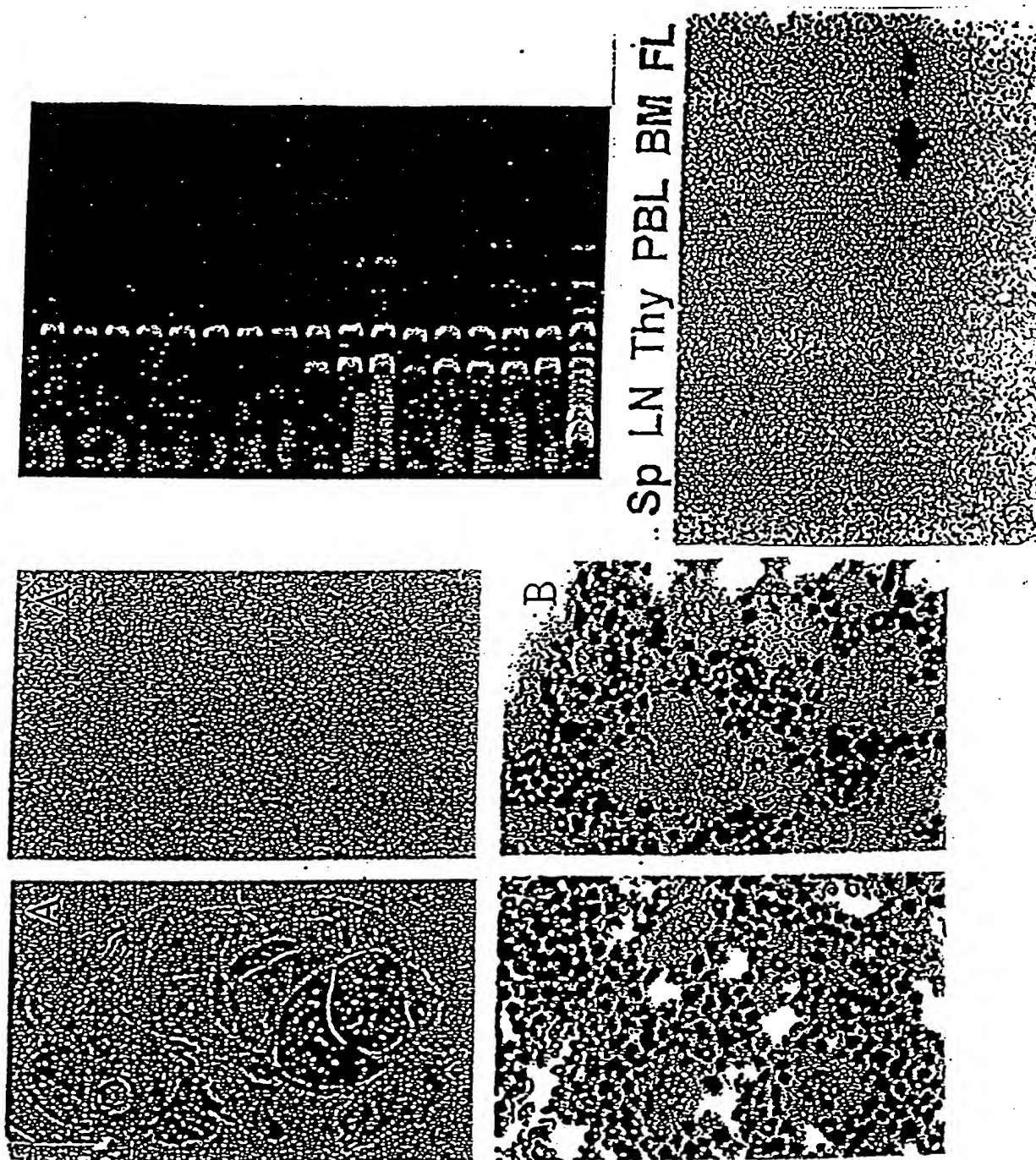


FIGURE 14

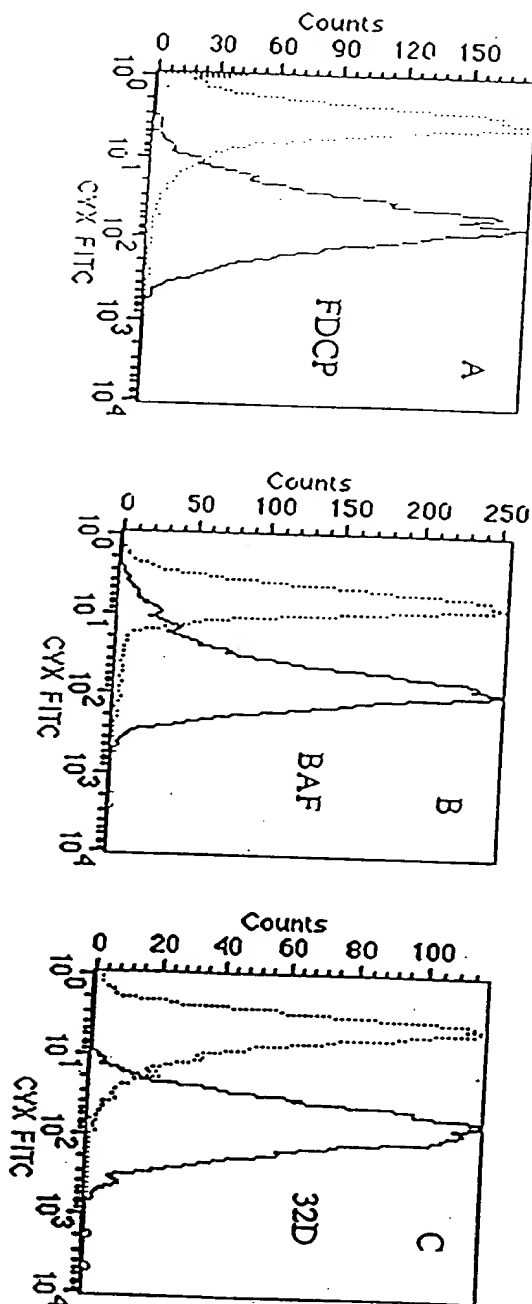


FIGURE 15

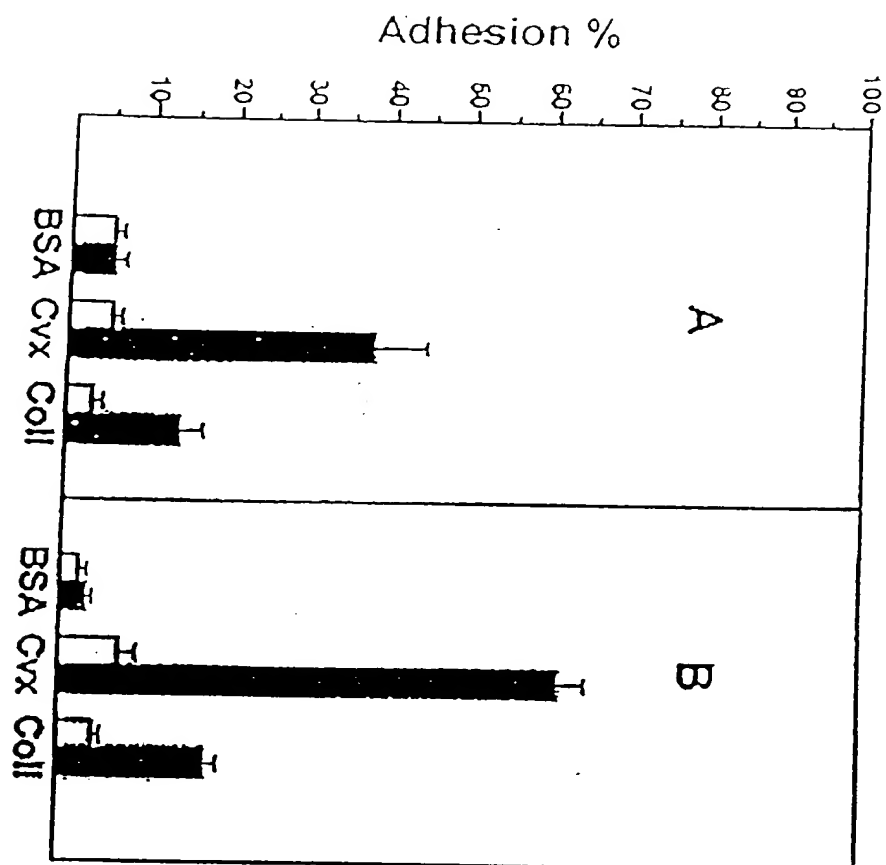


FIGURE 16

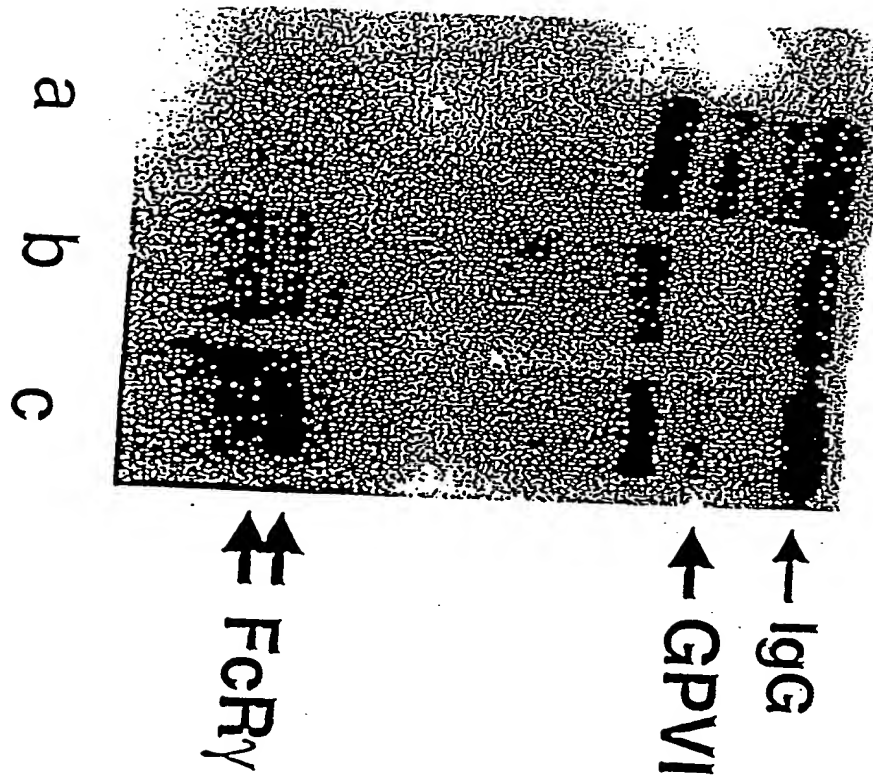


FIGURE 17

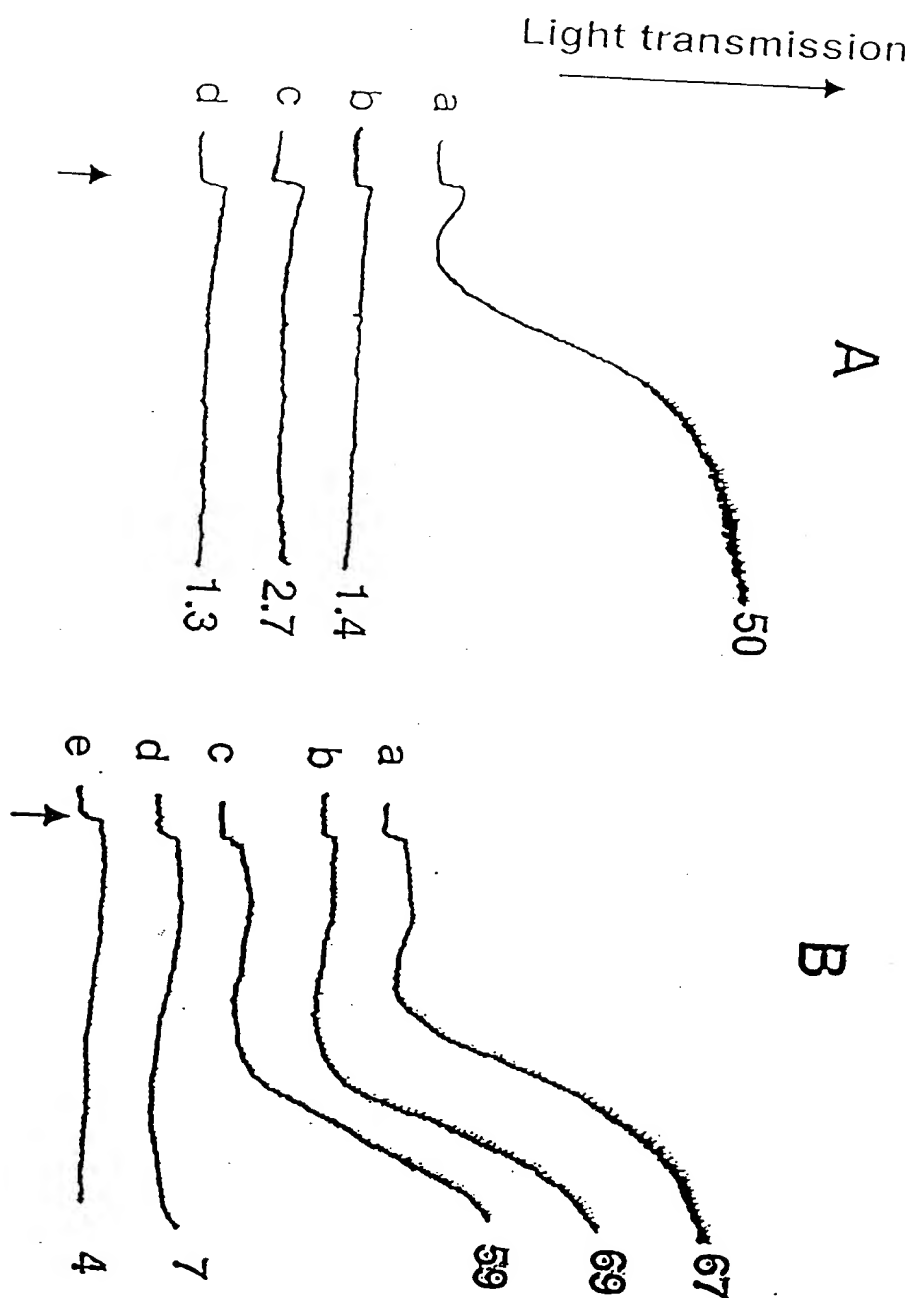


FIGURE 18

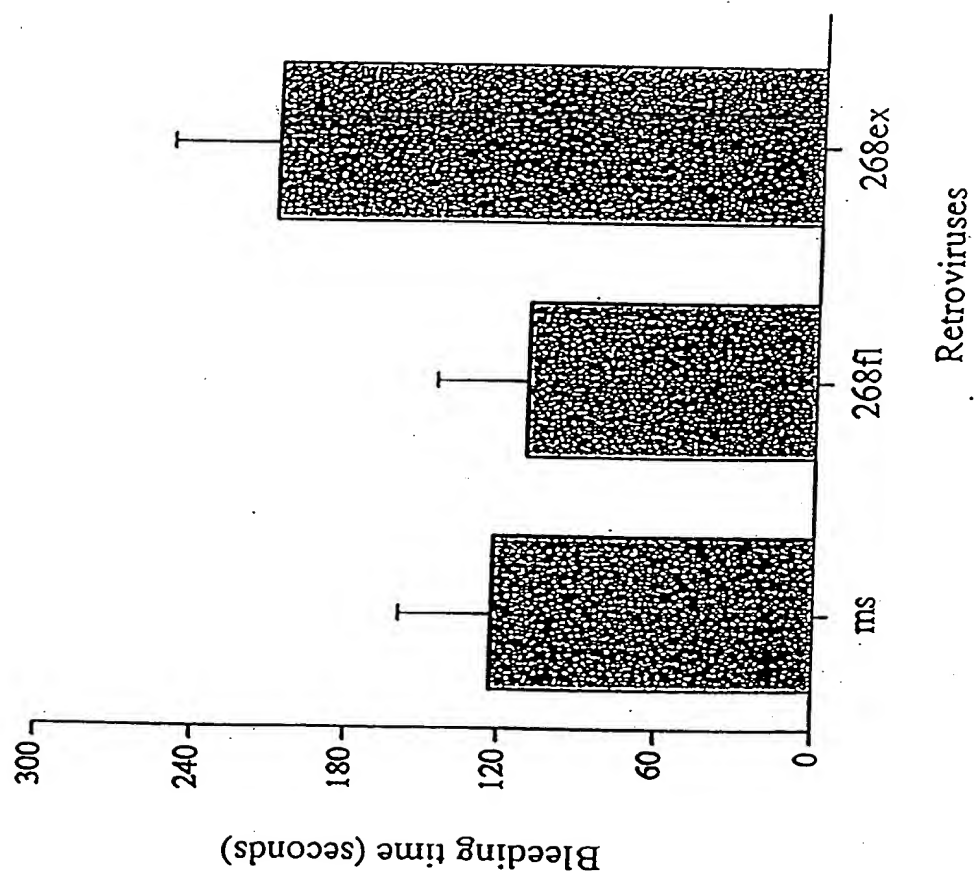


FIGURE 19

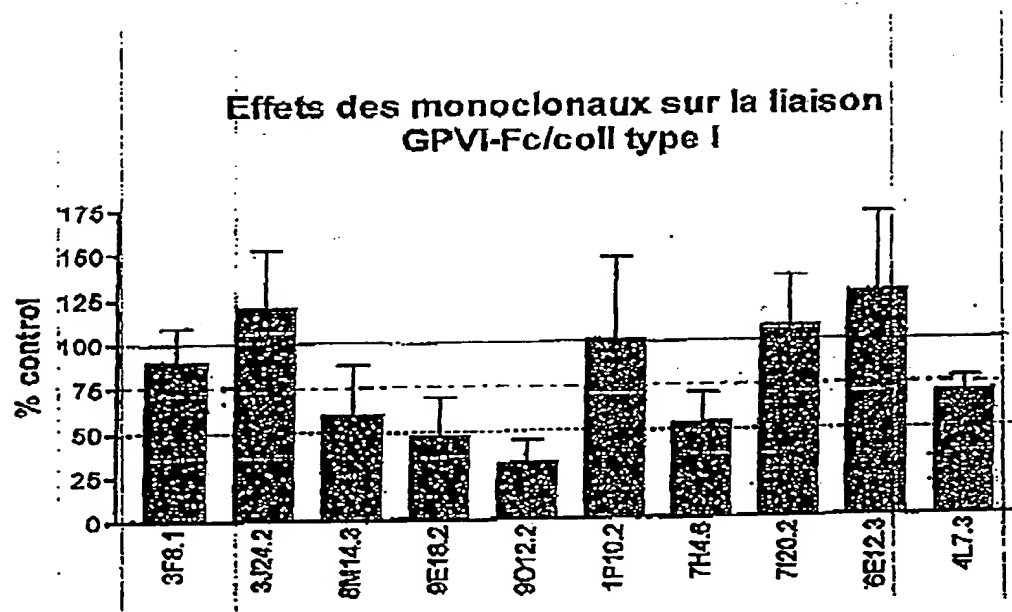


FIGURE 20

Effet des monoclonaux sur la liaison
GPR-fc / Convolvine

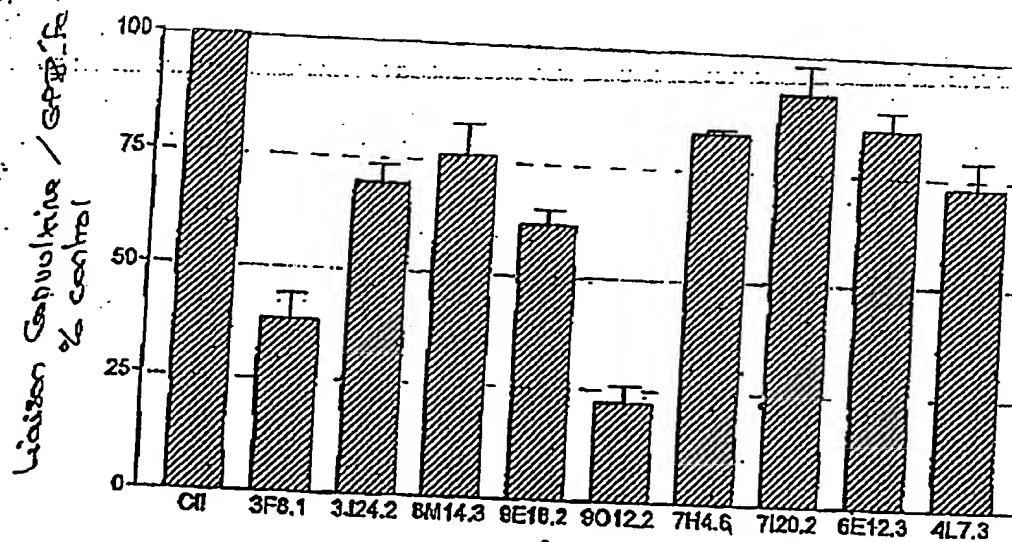
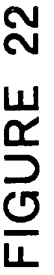


FIGURE 21



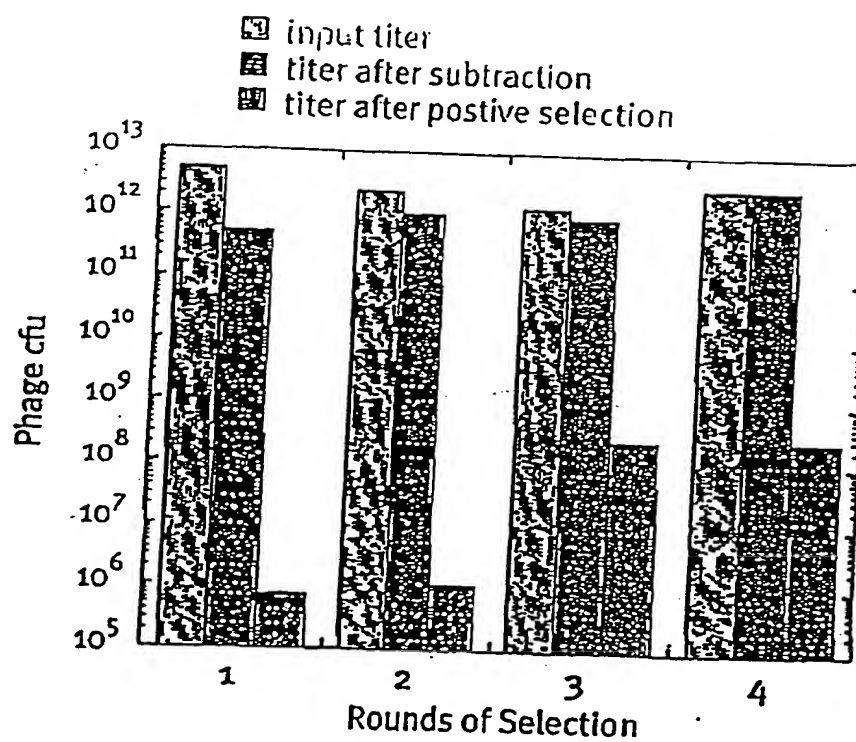


FIGURE 23

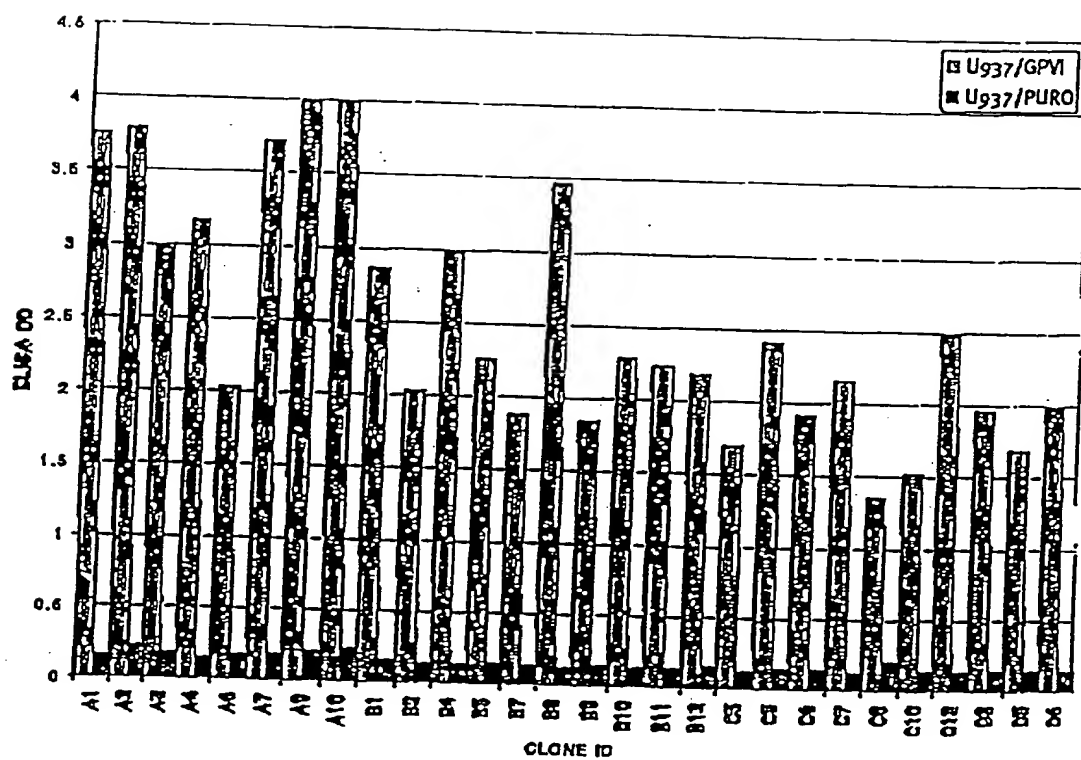


FIGURE 24a

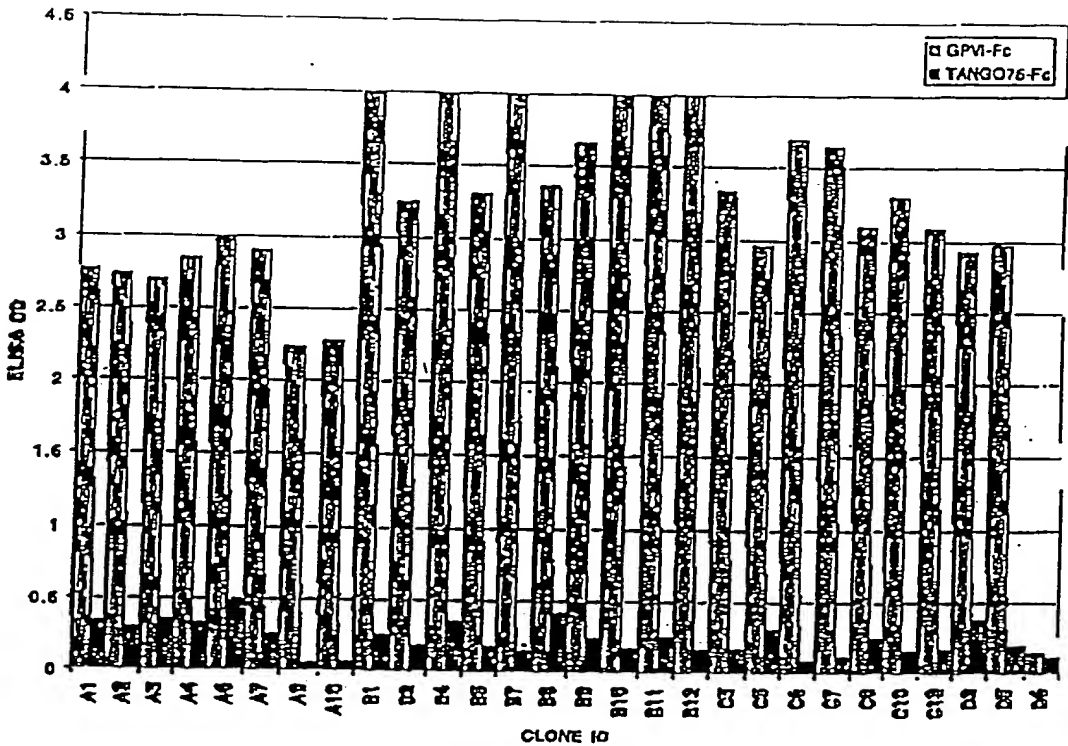


FIGURE 24b

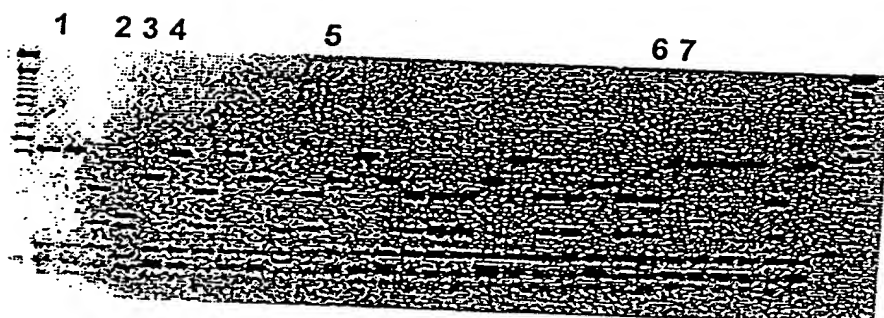
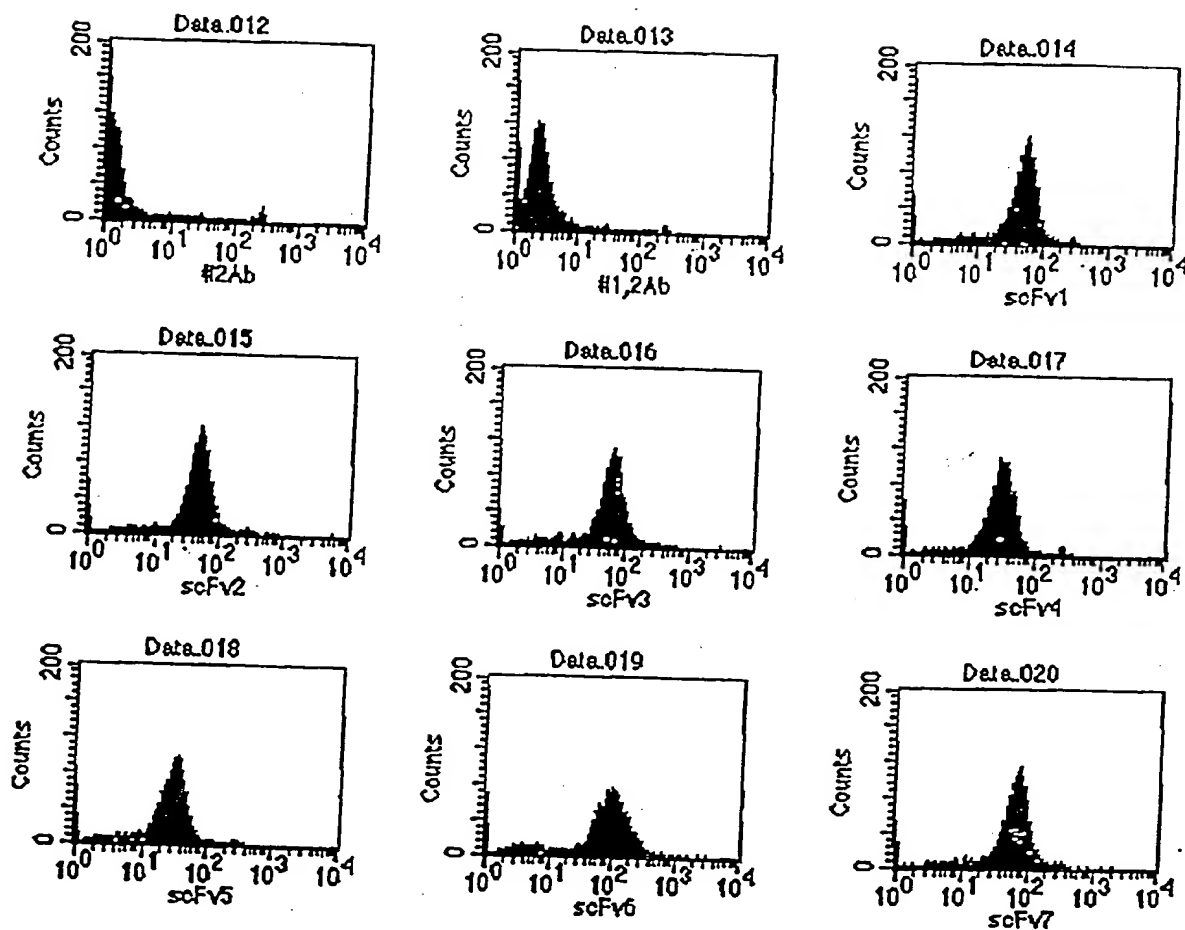


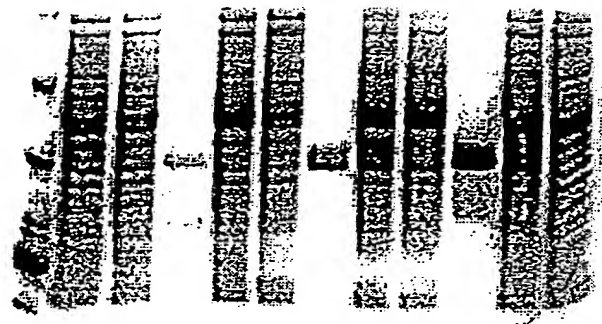
FIGURE 25



scFv1:A4
scFv2:B4
scFv3:A9
scFv4:C3
scFv5:C9
scFv6:C10
scFv7:A10

FIGURE 26

A4 A9 A10



B4 C3 C9 C10



FIGURE 27

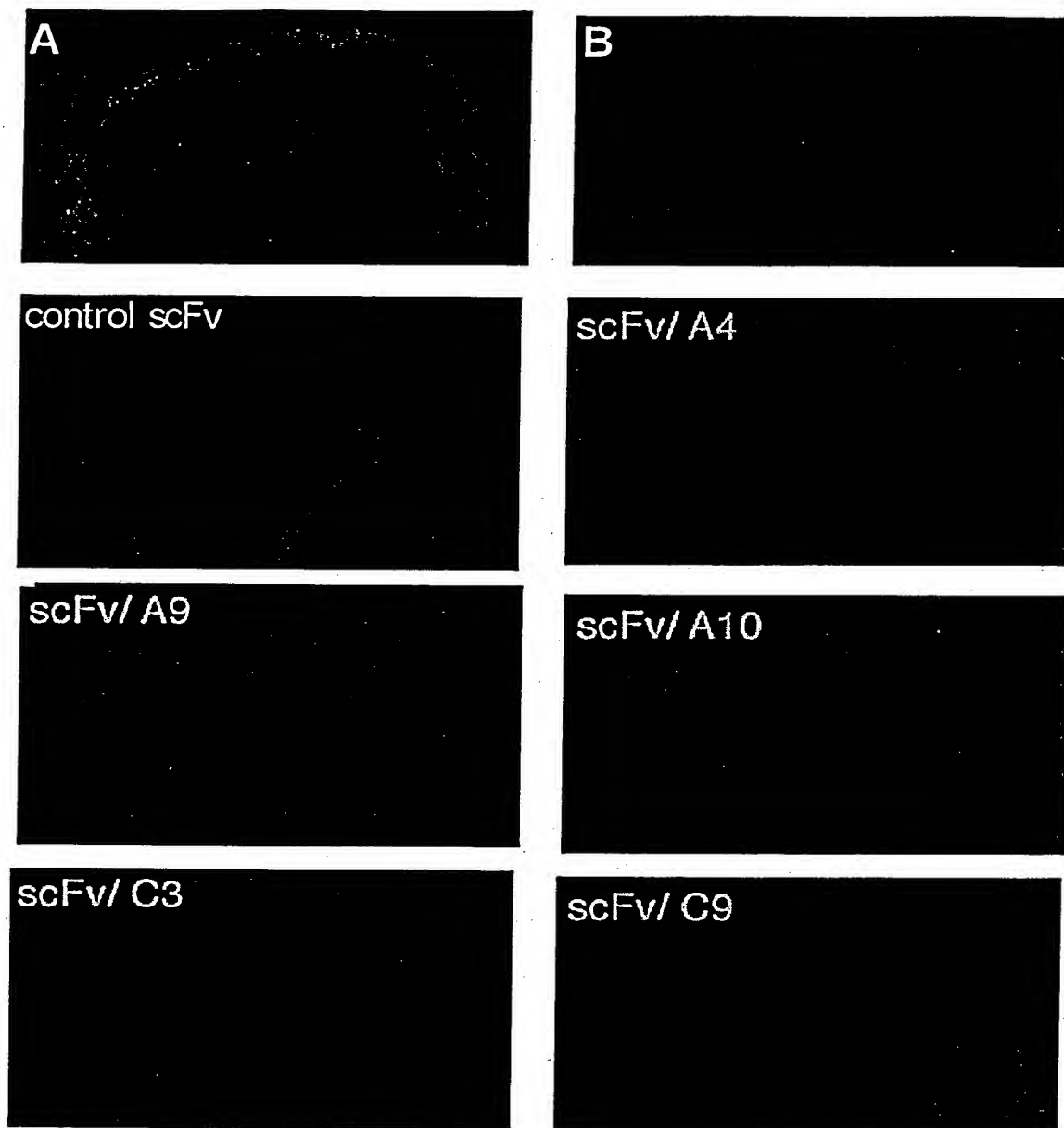


FIGURE 28

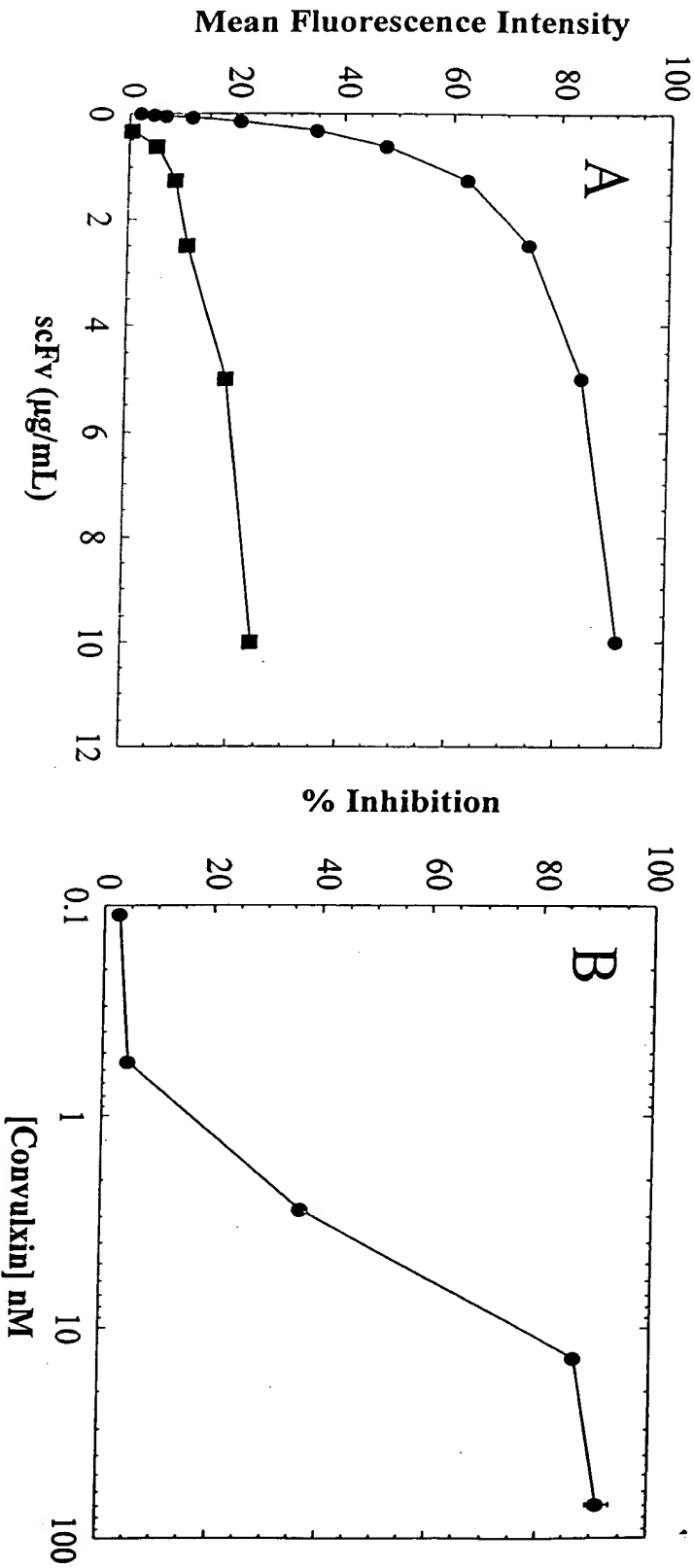


FIGURE 29

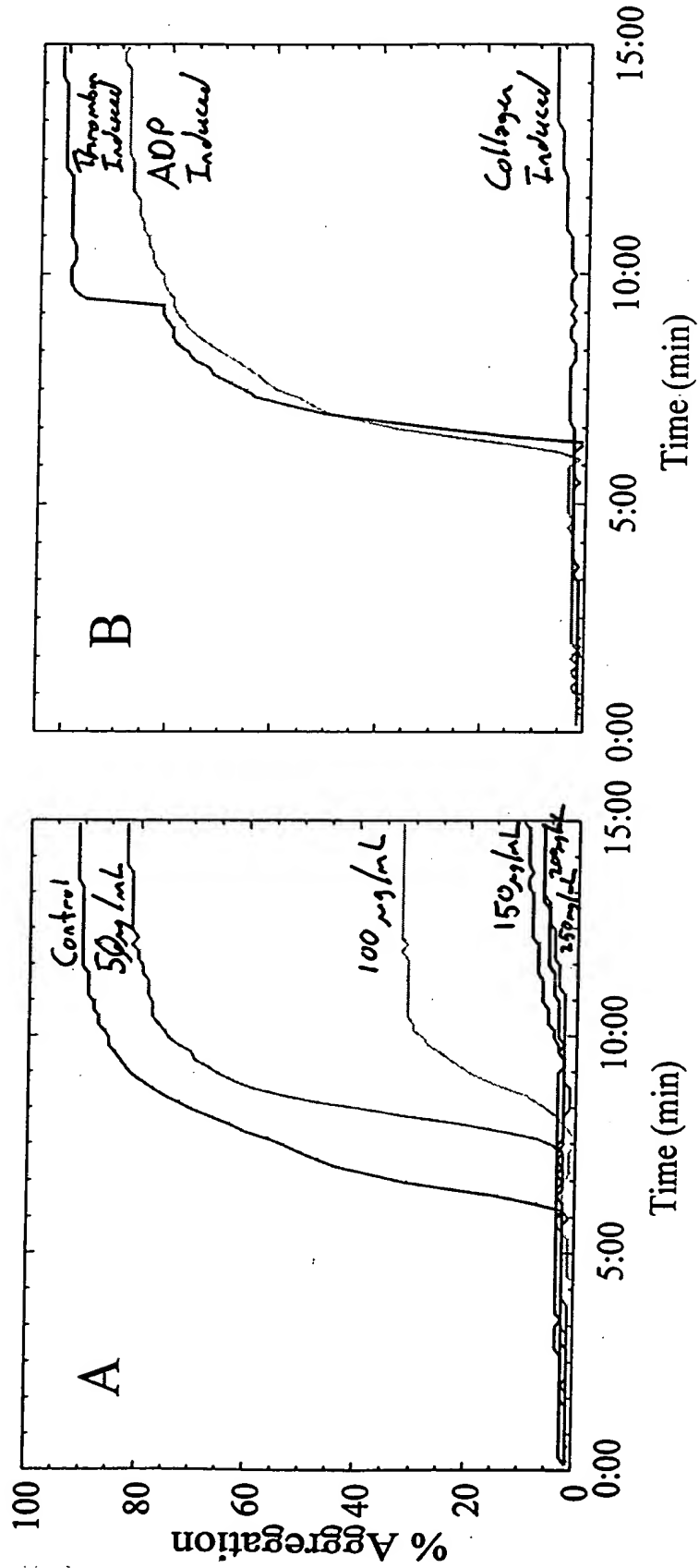


FIGURE 30